

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:10:44 ; Search time 32.86 Seconds

(without alignments)
113.650 Million cell updates/sec

Title: us-09-331-631a-25_copy_31_85

Sequence: 1 ENPKHNKCLQSCNSERSDYR.....EECEGEIPRRPRQHPER 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_66:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	100.0	605	1 FMSYBA	beta-conglycinin a
2	315	100.0	605	2 S20007	beta-conglycinin a
3	259.5	82.4	639	2 B24810	alpha-conglycinin a
4	65.5	20.8	774	2 T39539	alpha-amylase homo
5	63.5	20.2	373	2 T21955	hypothetical prote
6	63.5	20.2	414	2 T21954	hypothetical prote
7	63	20.0	663	2 T26835	hypothetical prote
8	62.5	19.8	588	1 FWCNAB	alpha-globulin B p
9	62.5	19.8	3051	2 S42373	hypothetical prote
10	62	19.7	389	2 T49640	transcription fact
11	62	19.7	390	2 S44285	EAR2 protein - mou
12	62	19.7	462	2 T00708	violaxanthin de-ep
13	61	19.4	147	2 T26225	hypothetical prote
14	61	19.4	1952	2 T48814	hypothetical prote
15	60	19.0	1646	2 JH0422	voltage-dependent
16	60	19.0	2203	2 T42742	voltage-dependent
17	59.5	18.9	174	2 B01C1T	Balbiant ring-1 ch
18	59	18.7	199	2 T28981	hypothetical prote
19	59	18.7	281	2 D29960	Balbiant ring 6 ch
20	59	18.7	344	2 S34153	msl101-1 protein -
21	59	18.7	713	2 A35502	major surface-labe
22	59	18.7	1390	2 S51364	sperm tail-specific
23	58.5	18.6	411	2 T51285	hepatocyte growth
24	58.5	18.6	1610	2 A46227	voltage-dependent
25	58	18.4	81	2 A43520	transglutaminase s
26	58	18.4	478	2 T03750	violaxanthin de-ep
27	58	18.4	798	2 S01659	integrin beta-1 ch
28	58	18.4	799	1 TJMSFB	fibronectin recept
29	58	18.4	799	2 JCA126	Integrin Beta O19

30	58	18.4	803	1 IJCH3	Integrin, band 3 p
31	58	18.4	2161	2 JH0564	calcium channel al
32	58	18.4	2181	2 A38198	calcium channel al
33	57.5	18.3	131	1 BGB02	spermatid transiti
34	57.5	18.3	179	2 S28256	NADH dehydrogenase
35	57.5	18.3	231	2 T14801	MADS box protein M
36	57.5	18.3	337	2 T27635	homeobox protein c
37	57.5	18.3	422	2 T51199	hypothetical prote
38	57.5	18.3	542	1 A54963	transcription fact
39	57.5	18.3	566	2 S22477	vicilin precursor
40	57.5	18.3	1300	2 A36502	insulin receptor-r
41	57	18.1	223	2 S43535	zev-2 protein - zeb
42	57	18.1	403	2 S02709	ear-2 protein - hu
43	57	18.1	511	2 S24345	Balbiant ring 1 pr
44	57	18.1	572	2 T29880	hypothetical prote
45	57	18.1	633	2 T47524	hypothetical prote

ALIGNMENTS

RESULT 1

FMSYBA
beta-conglycinin alpha chain precursor - soybean

C:Species: Glycine max (soybean)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jul-1999

C:Accession: S14681; S74124; S06714

R:Sebastiani, F.L.; Farrell, L.B.; Schuller, M.A.; Beachy, R.N.

Plant Mol. Biol. 15, 197-201, 1990

A:Title: Complete sequence of a cDNA of alpha subunit of soybean beta-conglycinin.

A:Reference number: S14681; MUID:91355860

A:Accession: S14681

A:Molecule type: mRNA

A:Residues: 1-605 <SEB>

A:Cross-references: EMBL:X17698; NID:g18535; PIDD:CA35691.1; PID:g18536

R:Shutov, A.D.; Kakhovskaya, I.A.; Bestyagina, A.S.; Bulnaga, V.P.; Horstmann, C.; Mu

Eur. J. Biochem. 241, 221-228, 1996

A:Title: Limited proteolysis of beta-conglycinin and glycinin, the 7S and 11S storage

A:Reference number: S74123; MUID:97054613

A:Accession: S74124

A:Molecule type: protein

A:Residues: 189-196, 'H', 198, 'N', 200, 'X', 202-203; 397-408, 'X', 410, 'X', 412-417, 'X', 419-4

A:Experimental source: seed

C:Superfamily: glycinin

C:Keywords: glycoprotein; seed; storage protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-65/Domain: propeptide #status predicted <PRO>

F:63-605/Product: beta-conglycinin alpha chain #status predicted <MAT>

F:261,517/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 315; DB 1; Length 605;

Best local Similarity 100.0%; Pred. No. 1,1e-26;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPKHNKCLQSCNSERSDYRQACIARCNLKYKECEGEIIPRRPRQHPER 55
Db 31 ENPKHNKCLQSCNSERSDYRQACIARCNLKYKECEGEIIPRRPRQHPER 85

RESULT 2

S20007
beta-conglycinin alpha chain precursor - soybean

C:Species: Glycine max (soybean)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S20007

R:Lelievre, J.M.; Dickinson, C.D.; Dickinson, L.A.; Nielsen, N.C.

Plant Mol. Biol. 18, 259-274, 1992

A:Title: Synthesis and assembly of soybean beta-conglycinin in vitro.

A:Reference number: S20007; MUID:92119248

A:Accession: S20007

A>Status: preliminary

A:Molecule type: mRNA

C:Superfamily: unassigned erba-related proteins: erba transforming protein homology
C:Keywords: zinc finger
F:55-300/Domain: erba transforming protein homology <ERBA>

Query Match 19.7%; Score 62; DB 2; Length 390;

Best Local Similarity 33.3%; Pred. No. 16;

Matches 16; Conservative 6; Mismatches 18; Indels 8; Gaps 2;

Db 92 TCRSRRCCQIDQHHRRNCQYCRLLKCKFRVGRKRAVGRGRIPHALPGR 139

RESULT 12

T00708

violaxanthin de-epoxidase homolog F22013.3 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999

C:Accession: T00708

R:Shim, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Col
eologis, A.; Ecker, J.R.

Submitted to the EMBL Data Library, April 1998

A:Description: Genomic sequence for Arabidopsis thaliana BAC F22013.

A:Reference number: Z14200

A:Accession: T00708

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-462 <SHI>

A:Cross-references: EMBL:AC003981; NID:g3063438; PID:g3063441; GSPDB:GN00059; ATSP:F2201
C:Experimental source: cultivar Columbia

A:Gene: ATSP:F22013.3

A:Map position: 1

A:Introns: 72/3; 128/2; 160/3; 292/2

Query Match 19.7%; Score 62; DB 2; Length 462;

Best Local Similarity 27.6%; Pred. No. 19;

Matches 16; Conservative 7; Mismatches 15; Indels 20; Gaps 3;

Db 8 CLOCSNRSYRNQACHRC-----NLKVEKEEC-----EGEIPRRPP 48

146 CLOTCNNRPD---ETECQICGDLFENSVDYDERNECAVSKKCVPRKSDLGEPAPDP 200

RESULT 13

T26225

hypothetical protein W06D11.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T26225

R:Lloyd, C.

Submitted to the EMBL Data Library, February 1996

A:Reference number: Z20176

A:Accession: T26225

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-147 <WIL>

A:Cross-references: EMBL:Z69718; PIDN:CAA93537.1; GSPDB:GN00028; CESP:W06D11.5

A:Experimental source: clone W06D11

C:Genetics:

A:Gene: CESP:W06D11.5

A:Map position: X

A:Introns: 103/3

Query Match 19.4%; Score 61; DB 2; Length 147;

Best Local Similarity 40.9%; Pred. No. 8.9;

Matches 18; Conservative 4; Mismatches 18; Indels 4; Gaps 1;

Db 9 LOCNSRDSYRNQACHRCNLKVEKEEC-----EGEIPRRPP 48

Db 50 LMSCLSRRESFVLQEVKRDQMLKVGILKICNEMWLQEGNSNRPP 93

RESULT 14

T48814

hypothetical protein 15E6.220 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000

C:Accession: T48814

R:Schulze, U.; Allyn, V.; Hehse, J.; Brandt, P.; Farthmann, B.; Holland, R.; Nyakatu

Submitted to the Protein Sequence Database, April 2000

A:Reference number: Z24541

A:Accession: T48814

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1952 <SCB>

A:Cross-references: EMBL:AL353822; GSPDB:GN00112; NCSP:15E6.220

A:Experimental source: cosmid contig 15E6; strain 74

C:Genetics:

A:Gene: NCSP:15E6.220

A:Map position: 2

A:Introns: 281/3

Query Match 19.4%; Score 61; DB 2; Length 1952;

Best Local Similarity 24.7%; Pred. No. 85;

Matches 18; Conservative 16; Mismatches 19; Indels 20; Gaps 3;

Db 2 NPKKNCLOCSNRSYRNQACH-----ARCNLKVKEKEEC-----G 41

585 SPEDNEVMSVDPDQDSQSELPDEDILPDAPDHVETVEKEAEDDDDEARSQS 644

Db 42 EIPRRPPQHP 54

Db 645 QSVKPEPRPEPD 657

RESULT 15

JH0422

voltage-dependent calcium channel complex alpha-1 chain - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Jan-2000

C:Accession: JH0422; D35901; I60901

R:Hu, A.; Ellinor, P.T.; Krizanov, O.; Wang, J.J.; Diebold, R.J.; Schwartz, A.

Neuron 7, 35-44, 1991

A:Title: Molecular cloning of multiple subtypes of a novel rat brain isoform of the a

A:Reference number: JH0422; MUID:9129338

A:Accession: JH0422

A:Molecule type: mRNA

A:Residues: 1-1646 <HU1>

A:Cross-references: GB:M57682; NID:g206573; PIDN:AAA42015.1; PID:g206574

A:Experimental source: brain

R:Snutch, T.P.; Leonard, J.P.; Gilbert, M.M.; Lester, H.A.; Davidson, N.

Proc. Natl. Acad. Sci. U.S.A. 87, 3391-3395, 1990

A:Title: Rat brain expresses a heterogeneous family of calcium channels.

A:Reference number: A35901; MUID:90239020

A:Accession: D35901

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA

A:Residues: 1247-1434 <SN2>

A:Experimental source: brain

R:Yu, A.S.L.; Hebert, S.C.; Brenner, B.M.; Lytton, J.

Proc. Natl. Acad. Sci. U.S.A. 89, 10494-10498, 1992

A:Title: Molecular characterization and nephron distribution of a family of transcrip

A:Reference number: A46422; MUID:93066265

A:Accession: I60901

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1040-1261,1305-1365 <RES>

A:Cross-references: GB:M99221; NID:g203370; PIDN:AAA0895.1; PID:g203371

A:Experimental source: kidney

C:Comment: Calcium channels are essential for many cellular functions, such as muscle

n.

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
 C:Keywords: alternative splicing; calcium binding; calcium channel; glycoprotein; phosph
 F:1463-1491/Domain: calcium binding #status predicted <EFC>
 F:154,224,328/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:464,848,1489,1584/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 19.0%; Score 60; DB 2; Length 1646;
 Best local similarity 34.9%; Pred. No. 94;
 Matches 22; Conservative 9; Mismatches 18; Indels 14; Gaps 4;
 QY 1 ENPKHNK--CLOCSNSER---DSTRNOA---CHARCNLLKVEKECEGEGLR---P 46
 DB 783 ENKKNNKPEVNOIANSNDKVTIDYQEEAEKDPYPPCDVPVCGEEEEEDEDEPEVPAGP 842
 QY 47 RPR 49
 DB 843 RPR 845

Search completed: March 1, 2001, 16:10:46
 Job time: 1077 sec

